

- 1 -

```
piece 1, NC_000913, metA_aceB-, config: linear, direction: -, begin: 4213530, end: 4213213
```

*4213530 * *4213520 * *4213510 * *4213500 * *4213490 * *4213480 * *4213470 * *4213460 * *4213450
 5' t t c a t c g g t t g t t g c t g t t c a g t c a t c g t g c a g t c c t c g t a c t g g a a a a c t t c c c a c t g g a a c g a a g g a 3'
 - phe - ile - gly - cys - cys - leu - phe - ser - his - arg - ala - ala - pro - arg - his - gly - ser - glu - asn - phe - pro - thr - val - asn - glu - gly -
 - ser - ser - val - val - ala - cys - ser - val - ile - val - gln - leu - leu - val - met - asp - pro - lys - thr - ser - pro - leu - ● - - - -
 - his - arg - leu - leu - leu - pro - val - gln - ser - ser - ser - ser - trp - ile - arg - lys - leu - pro - his - cys - glu - arg - arg - ile -
 ...] NC_000913.aceB

... ----- } p35-(26)-p10 4213358 Gap 3.7 bits

Diagram illustrating the structure of the 4213282 metA gene. The gene is oriented 5' to 3' from left to right. Key features include:

- Promoters:** Indicated by red circles above the sequence.
- Start Sites:** Indicated by asterisks (*).
- Codons:** Shown below the sequence in green, blue, and red.
- orf 24 codons:** A bracketed region starting at the first promoter.
- orf 7 codons:** A bracketed region starting after the first gap.
- sd-(10)-ir 4213282 Gap 2.7 bits:** A bracketed region indicating a gap between the two orfs.
- sd-ir 4213282 metA aceB- total 5.1 bits:** A bracketed region indicating the total length of the intergenic region.
- ir metA_aceB-:** An inverted repeat sequence at the bottom.